I. AMENDMENT

IN THE SPECIFICATION:

Page 11, please delete the whole paragraph extending from line 5 to line 20 and replace it with the following new paragraph:

Accordingly, each target may be prepared from a set of cell dishes by isolation of RNA over a course of time. ~~The treatment of those cells may be emulated by adding, for example, serum thereto.~~ <u>Serum, for example, may be added to the cells in order to ensure a proper growth environment.</u> At predetermined intervals, a small amount of the fluid is removed, and the cells are put in a quiescent state to stop the reaction time. Accordingly, a large set of targets, having a predetermined amount of liquid (e.g., .5 ml each) is produced. The GeneChip™ fluidics station will then automatically hybridize each target, i.e., it will extract all the RNA and label the RNA by adding a chemical tag to each molecule, and control the delivery of the resulting liquid to the probe arrays to facilitate obtaining sequencing information regarding the mRNAs. This is done by the probe arrays exposing the target to light at a predetermined location and measuring the photons collected at various locations within the arrays. The amount of mRNA is then ascertained based upon the signal strength of the reading given by the probe at the appropriate location corresponding to that sequence or sequence segment. A net change in signal may indicate activation or repression of gene transcription, or possibly post-transcriptional stabilization the mRNA due a given set of treatment conditions.

Page 12, please delete the whole paragraph extending from line 14 to line 21 and replace it with the following new paragraph:

Public domain GeneChip® data describing the yeast cell cycle (downloaded from
~~http://genomics.stanford.edu~~ a Stanford online genomics database) was chosen to validate the
fuzzy logic algorithm. Since the yeast cell cycle is a tightly regulated process at the genetic
level, the expression data was expected to show detectable relationships among different
genes that might be detected via a fuzzy logic algorithm. Also, years of experimental work
on yeast has generated an extensive body of biological data describing many of the proteins
in the organism, allowing the confirmation or dismissal of findings based on data in the
literature.

*Please delete the whole paragraph extending from line 22 on page 12 to line 7 on
page 13 and replace it with the following new paragraph:*

In this illustrated embodiment, at S20, GeneChip® data were obtained from a set of 17
experiments in which data points were profiled under various biological conditions. Thus,
the relationship between proteins in numerous distinct cell types and under various stress
conditions were followed to ensure detected relationships between gene products were not the
results of an artifact created under a particular experimental condition. Each individual
experimental condition was repeated 2 or 3 times, and the averaged results were included as a
single experiment in the set of 17 experiments analyzed. All proteins later evaluated for
relationship purposes must have been expressed to some measurable degree under all 17
experimental conditions. Preferably, a minimum of 9 experimental conditions should be
included, although this is not absolute. No maximum number of experiments is controlling.

Page 19, please delete the whole paragraph extending from line 13 to line 18 and replace it with the following new paragraph:

In order to evaluate and validate the algorithm, the best scoring triplets were examined to assess their biological relevance.[[.]] One of the best scoring triplets, CYB2-HAP1-CYC7, is shown in Figure 3., wherein the top panel shows a correlation of the predicted and the observed values for CYC1 (C), while the middle panel shows the relationship of CYB2 (A) and HAP1 (B), and the bottom panel depicts the relationship of CYB2 (A) and CYC1 (C).

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